

# SCORE Search Results Details for Application 10724274 and Search Result us-10-724-274-7.rup.

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This page gives you Search Results detail for the Application 10724274 and Search Result us-10-724-274-7.rup.

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:36:54 ; Search time 296 Seconds  
(without alignments)  
340.631 Million cell updates/sec

Title: US-10-724-274-7  
Perfect score: 566  
Sequence: 1 QIVLTQSPAIMASASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	484	85.5	114	2	Q8K1F1_MOUSE	Q8k1f1 mus musculu
2	469.5	83.0	131	2	Q811C3_MOUSE	Q811c3 mus musculu
3	462	81.6	134	2	Q8VDD0_MOUSE	Q8vdd0 mus musculu
4	459	81.1	106	2	Q2VR04_MOUSE	Q2vr04 mus musculu
5	454	80.2	106	2	Q2VT27_MOUSE	Q2vt27 mus musculu
6	452	79.9	112	2	Q8K1F3_MOUSE	Q8k1f3 mus musculu
7	445	78.6	112	2	Q8K1F2_MOUSE	Q8k1f2 mus musculu

8	441	77.9	106	2	Q2VT29_MOUSE	Q2vt29	mus	musculu
9	441	77.9	112	2	Q8K1F0_MOUSE	Q8k1f0	mus	musculu
10	441	77.9	235	2	Q58EV6_MOUSE	Q58ev6	mus	musculu
11	439	77.6	106	2	Q2VT25_MOUSE	Q2vt25	mus	musculu
12	434	76.7	237	2	Q569Y8_MOUSE	Q569y8	mus	musculu
13	432	76.3	107	1	KV6F_MOUSE	P04940	mus	musculu
14	429	75.8	235	2	Q5XFY8_MOUSE	Q5xfy8	mus	musculu
15	427	75.4	107	1	KV6I_MOUSE	P04943	mus	musculu
16	426	75.3	107	1	KV6H_MOUSE	P04942	mus	musculu
17	426	75.3	237	2	Q3KQK1_MOUSE	Q3kqk1	mus	musculu
18	423	74.7	107	1	KV6G_MOUSE	P04941	mus	musculu
19	422	74.6	107	1	KV6J_MOUSE	P04944	mus	musculu
20	418	73.9	129	1	KV4A_MOUSE	P01680	mus	musculu
21	416	73.5	107	1	KV6D_MOUSE	P01678	mus	musculu
22	415	73.3	107	1	KV6A_MOUSE	P01675	mus	musculu
23	415	73.3	108	1	KV6K_MOUSE	P04945	mus	musculu
24	414	73.1	106	2	Q9U410_MOUSE	Q9u410	mus	musculu
25	410	72.4	107	1	KV6B_MOUSE	P01676	mus	musculu
26	408	72.1	107	1	KV6C_MOUSE	P01677	mus	musculu
27	403	71.2	107	1	KV6E_MOUSE	P01679	mus	musculu
28	394.5	69.7	236	2	Q6PIH7_HUMAN	Q6pih7	homo	sapien
29	388.5	68.6	101	2	Q9JL78_MOUSE	Q9jl78	mus	musculu
30	387.5	68.5	97	2	Q9JL76_MOUSE	Q9jl76	mus	musculu
31	382	67.5	109	2	Q9UL78_HUMAN	Q9ul78	homo	sapien
32	376.5	66.5	108	2	Q9UL79_HUMAN	Q9ul79	homo	sapien
33	373	65.9	129	1	KV3L_HUMAN	P18135	homo	sapien
34	371.5	65.6	111	1	KV3T_MOUSE	P01672	mus	musculu
35	369.5	65.3	108	2	Q9UL77_HUMAN	Q9ul77	homo	sapien
36	369	65.2	109	1	KV3F_HUMAN	P01624	homo	sapien
37	366.5	64.8	111	1	KV3J_MOUSE	P01662	mus	musculu
38	366.5	64.8	111	1	KV3R_MOUSE	P01670	mus	musculu
39	366	64.7	107	2	Q96SA9_HUMAN	Q96sa9	homo	sapien
40	365.5	64.6	108	2	Q9UL70_HUMAN	Q9ul70	homo	sapien
41	365.5	64.6	111	2	Q920E9_MOUSE	Q920e9	mus	musculu
42	365.5	64.6	131	1	KV3I_MOUSE	P01661	mus	musculu
43	365	64.5	109	2	Q9UL85_HUMAN	Q9ul85	homo	sapien
44	365	64.5	129	1	KV3M_HUMAN	P18136	homo	sapien
45	364	64.3	109	1	KV3B_HUMAN	P01620	homo	sapien

## ALIGNMENTS

## RESULT 1

## Q8K1F1\_MOUSE

ID Q8K1F1\_MOUSE PRELIMINARY; PRT; 114 AA.

AC Q8K1F1;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE Anti-VIPase light chain variable region (Fragment).

GN Name=Gml418;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

# SCORE Search Results Details for Application 10724274

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GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:40:24 ; Search time 39 Seconds  
(without alignments)  
268.914 Million cell updates/sec

Title: US-10-724-274-7  
Perfect score: 566  
Sequence: 1 QIVLTQSPAIMASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	485	85.7	99	2	PH1058	Ig light chain V r
2	484	85.5	130	2	A32513	Ig kappa chain pre
3	479	84.6	99	2	PH1059	Ig light chain V r
4	467	82.5	99	2	PH1060	Ig light chain V r
5	460	81.3	130	2	S04573	Ig kappa chain pre
6	457	80.7	105	2	S26338	Ig kappa chain V r
7	456.5	80.7	108	2	G30560	Ig kappa chain V r
8	456	80.6	113	2	S03410	Ig kappa chain pre

9	455	80.4	107	2	A30562	Ig kappa chain V r
10	455	80.4	140	2	PL0013	Ig kappa chain pre
11	453	80.0	130	2	B32456	Ig kappa chain pre
12	451	79.7	107	2	PC4405	Ig kappa chain V r
13	450	79.5	107	2	B30562	Ig kappa chain V r
14	445	78.6	108	2	PL0278	Ig kappa chain V r
15	441	77.9	108	2	PL0277	Ig kappa chain V r
16	441	77.9	108	2	PL0276	Ig kappa chain V r
17	439	77.6	130	1	JL0079	Ig kappa chain pre
18	437	77.2	106	2	PL0082	Ig kappa chain V r
19	436	77.0	123	2	S05269	Ig kappa chain pre
20	435	76.9	106	2	PS0071	Ig kappa chain V r
21	434	76.7	106	2	B54378	Ig light chain V r
22	434	76.7	109	2	PT0405	Ig light chain V r
23	433.5	76.6	108	2	S38720	Ig light chain V r
24	433	76.5	106	2	G27887	Ig kappa chain V r
25	432	76.3	107	2	PT0406	Ig kappa chain V r
26	431	76.1	104	2	B49049	Ig kappa chain V r
27	430	76.0	103	2	S29591	Ig kappa chain V r
28	429	75.8	107	2	PD0011	Ig kappa chain V r
29	429	75.8	108	2	PS0069	Ig kappa chain V r
30	428	75.6	235	2	S25058	Ig kappa chain - m
31	427	75.4	120	2	S66536	Ig light chain V r
32	426	75.3	96	2	C33730	Ig kappa chain V r
33	425	75.1	109	2	S13699	Ig kappa chain V r
34	425	75.1	124	2	S05267	Ig kappa chain pre
35	424	74.9	108	2	S29581	Ig kappa chain V r
36	423	74.7	107	2	S11119	Ig kappa chain V r
37	422.5	74.6	98	2	PH1061	Ig light chain V r
38	422	74.6	107	2	A42848	Ig light chain V r
39	422	74.6	109	2	PT0404	Ig light chain V r
40	421	74.4	100	2	S29590	Ig kappa chain V r
41	421	74.4	107	2	S11118	Ig kappa chain V r
42	419	74.0	104	2	JC6076	anti-D-dimer monoc
43	419	74.0	106	2	S29583	Ig kappa chain V r
44	418	73.9	129	1	KVMS7B	Ig kappa chain pre
45	415	73.3	107	1	KVMSX4	Ig kappa chain V r

## ALIGNMENTS

## RESULT 1

PH1058  
 Ig light chain V region (clone 163.72) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
 C;Accession: PH1058  
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimul.  
 A;Reference number: PH0971; MUID:92381444; PMID:1512540  
 A;Accession: PH1058  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-99  
 A;Cross-references: UNIPROT:Q8K1F1; UNIPARC:UPI00001767C0  
 A;Experimental source: B cell, strain [NZB x NZW]F1  
 C;Superfamily: immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;16-91/Domain: immunoglobulin homology

# SCORE Search Results Details for Application 10724274 and Search Result us-10-724-274-7.rai.

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:45:24 ; Search time 51 Seconds  
(without alignments)  
187.075 Million cell updates/sec

Title: US-10-724-274-7  
Perfect score: 566  
Sequence: 1 QIVLTQSPAIMASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	511	90.3	244	US-08-230-843-2	Sequence 2, Appli
2	511	90.3	244	US-08-636-936-2	Sequence 2, Appli

3	505	89.2	231	1	US-08-681-432-1	Sequence 1, Appli
4	474	83.7	110	2	US-09-726-219A-256	Sequence 256, App
5	474	83.7	110	2	US-09-196-522-256	Sequence 256, App
6	472	83.4	110	2	US-09-726-219A-237	Sequence 237, App
7	472	83.4	110	2	US-09-196-522-237	Sequence 237, App
8	471	83.2	110	2	US-09-726-219A-257	Sequence 257, App
9	471	83.2	110	2	US-09-196-522-257	Sequence 257, App
10	463	81.8	110	2	US-09-726-219A-254	Sequence 254, App
11	463	81.8	110	2	US-09-196-522-254	Sequence 254, App
12	463	81.8	215	7	5455030-3	Patent No. 5455030
13	460	81.3	108	2	US-08-881-037-74	Sequence 74, Appl
14	459	81.1	129	1	US-08-116-778E-2	Sequence 2, Appli
15	459	81.1	129	1	US-08-438-562-2	Sequence 2, Appli
16	459	81.1	129	1	US-08-483-528B-92	Sequence 92, Appl
17	458	80.9	110	2	US-09-726-219A-255	Sequence 255, App
18	458	80.9	110	2	US-09-196-522-255	Sequence 255, App
19	456.5	80.7	214	2	US-09-653-755A-5	Sequence 5, Appli
20	455	80.4	107	2	US-08-783-853A-11	Sequence 11, Appl
21	455	80.4	107	2	US-09-344-050-11	Sequence 11, Appl
22	455	80.4	112	2	US-08-783-853A-103	Sequence 103, App
23	455	80.4	112	2	US-09-344-050-103	Sequence 103, App
24	453	80.0	108	2	US-09-726-219A-242	Sequence 242, App
25	453	80.0	108	2	US-09-196-522-242	Sequence 242, App
26	453	80.0	235	2	US-09-238-741-2	Sequence 2, Appli
27	452	79.9	128	1	US-08-476-275-4	Sequence 4, Appli
28	452	79.9	128	2	US-08-475-815B-7	Sequence 7, Appli
29	452	79.9	128	2	US-08-475-813-4	Sequence 4, Appli
30	451	79.7	129	1	US-08-449-287-2	Sequence 2, Appli
31	451	79.7	235	2	US-09-423-439-18	Sequence 18, Appl
32	451	79.7	235	2	US-09-423-439-58	Sequence 58, Appl
33	451	79.7	235	2	US-09-011-769A-23	Sequence 23, Appl
34	451	79.7	248	7	5455030-11	Patent No. 5455030
35	450	79.5	106	1	US-07-634-278-1	Sequence 1, Appli
36	450	79.5	106	1	US-07-634-278-16	Sequence 16, Appl
37	450	79.5	106	1	US-08-477-728-1	Sequence 1, Appli
38	450	79.5	106	1	US-08-477-728-16	Sequence 16, Appl
39	450	79.5	106	1	US-08-474-040-1	Sequence 1, Appli
40	450	79.5	106	1	US-08-474-040-16	Sequence 16, Appl
41	450	79.5	106	1	US-08-487-200-1	Sequence 1, Appli
42	450	79.5	106	1	US-08-487-200-16	Sequence 16, Appl
43	450	79.5	106	1	US-08-488-113B-163	Sequence 163, App
44	450	79.5	106	1	US-08-477-484B-163	Sequence 163, App
45	450	79.5	106	1	US-08-107-669D-49	Sequence 49, Appl

## ALIGNMENTS

## RESULT 1

US-08-230-843-2

; Sequence 2, Application US/08230843

; Patent No. 5582826

; GENERAL INFORMATION:

; APPLICANT: SHIMAMURA, TOSHIRO

; APPLICANT: HAMURO, JUNJI

; APPLICANT: NAKAZAWA, HARUMI

; APPLICANT: KANAYAMA, YUKA

; APPLICANT: SUGAMURA, KAZUO

; APPLICANT: TAKESHITA, TOSHIKAZU

; TITLE OF INVENTION: IMMUNOSUPPRESSANT

; NUMBER OF SEQUENCES: 12

SCORE Search Results Details for Application 10724274 and Search Result us-10-724-274-7.rag.

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:36:24 ; Search time 198 Seconds  
(without alignments)  
251.700 Million cell updates/sec

Title: US-10-724-274-7  
Perfect score: 566  
Sequence: 1 QIVLTQSPAIMASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	

1	566	100.0	109	8	ADT77625	Adt77625 IIA1 VL p
2	566	100.0	109	9	AEB51144	Aeb51144 Mouse ant
3	566	100.0	215	8	ADQ31885	Adq31885 Antibody
4	566	100.0	215	8	ADT77644	Adt77644 Antibody
5	566	100.0	215	9	AEB51163	Aeb51163 Chimeric
6	566	100.0	215	10	AEF12091	Aef12091 Anti-alph
7	566	100.0	215	10	AEF16423	Aef16423 Chimeric
8	564	99.6	215	8	ADT51708	Adt51708 M200 anti
9	561	99.1	130	8	ADQ31877	Adq31877 Antibody
10	561	99.1	130	8	ADQ31866	Adq31866 Murine an
11	561	99.1	130	8	ADQ31881	Adq31881 Antibody
12	561	99.1	130	8	ADT77640	Adt77640 Antibody
13	561	99.1	130	8	ADT77636	Adt77636 Antibody
14	561	99.1	130	9	AEB51155	Aeb51155 Chimeric
15	561	99.1	130	9	AEB51159	Aeb51159 Chimeric
16	561	99.1	130	9	AED49296	Aed49296 Anti-alph
17	561	99.1	130	9	AED49292	Aed49292 Anti-alph
18	534	94.3	110	8	ADT75068	Adt75068 Light cha
19	534	94.3	110	8	ADT75050	Adt75050 Light cha
20	533	94.2	109	10	AEF24398	Aef24398 Mouse mat
21	533	94.2	131	9	ADW14710	Adw14710 Monoclonal
22	533	94.2	131	10	AEF24378	Aef24378 Mouse PAN
23	524	92.6	110	9	AED34781	Aed34781 Chimeric
24	524	92.6	216	9	AED34778	Aed34778 Chimeric
25	522	92.2	131	9	ADW14791	Adw14791 Anti-KIR
26	521	92.0	110	9	ADW86132	Adw86132 Novel cyt
27	520	91.9	215	8	ADN97547	Adn97547 Artificia
28	520	91.9	483	8	ADN97549	Adn97549 Artificia
29	519	91.7	110	8	ADT75126	Adt75126 Light cha
30	518	91.5	108	3	AAB10021	Aab10021 H. pylori
31	518	91.5	110	8	ADT75052	Adt75052 Light cha
32	518	91.5	129	8	ADS94357	Ads94357 Antibody
33	517	91.3	108	8	ADT89037	Adt89037 Murine pl
34	517	91.3	113	10	AEG03168	Aeg03168 CD200 ant
35	512	90.5	108	3	AAY53591	Aay53591 Light cha
36	512	90.5	111	8	ADT75069	Adt75069 Light cha
37	511	90.3	111	8	ADT75060	Adt75060 Light cha
38	511	90.3	244	2	AAR60780	Aar60780 Fv (GP-2)
39	510	90.1	106	10	AEF02311	Aef02311 Mouse mon
40	510	90.1	109	9	AEA17138	Aea17138 Human TNF
41	509	89.9	112	6	ABJ19266	Abj19266 Anti-huma
42	509	89.9	282	6	ABJ19276	Abj19276 Anti-huma
43	507	89.6	109	8	ADQ31867	Adq31867 Humanised
44	507	89.6	109	8	ADT77626	Adt77626 1 VL pept
45	507	89.6	109	9	AEB51145	Aeb51145 Humanized

## ALIGNMENTS

## RESULT 1

## ADT77625

ID ADT77625 standard; peptide; 109 AA.

XX

AC ADT77625;

XX

DT 13-JAN-2005 (first entry)

XX

DE IIA1 VL peptide.

XX